

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 11, 2003, 01:59:12 ; Search time 68 Seconds
(without alignments)
327.251 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616

Sequence: 1 MAAMADVTPSGTNSGAGK.....KTRQVCPIDNREWEFOKYGH 108

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	4 Q9Y254	Q9Y254 homo sapien
2	616	100.0	108	11 Q9W0K9	Q9W0K9 mus musculu
3	605	98.2	108	11 Q9D1S2	Q9D1S2 mus musculu
4	604	98.1	189	13 Q8Q6G4	Q8Q6G4 salmo salar
5	534	86.7	108	5 Q9W5E1	Q9W5E1 drosophila
6	523.5	85.0	114	10 Q8S3S0	Q8S3S0 oryza sativ
7	514.5	83.5	118	10 Q940X7	Q940X7 arabidopsis
8	510	82.8	136	5 Q774Z9	Q774Z9 drosophila
9	499	81.0	115	10 Q9M2B0	Q9M2B0 arabidopsis
10	493	80.0	110	5 Q234S7	Q234S7 caenorhabdi
11	487.5	79.1	5	Q8W5Q1	Q8W5Q1 caenorhabdi
12	469	76.1	107	3 Q139S9	Q139S9 schizosacch
13	400.5	65.0	107	5 Q9NHX0	Q9NHX0 drosophila
14	400.5	65.0	122	5 Q9W0R1	Q9W0R1 drosophila
15	385	62.5	121	3 Q08273	Q08273 saccharomyc
16	378	61.4	107	5 Q77367	Q77367 plasmodium

17	314.5	51.1	97	10 Q9FTN1	Q9FTN1 oryza sativ
18	308	50.0	92	5 Q8SWJ6	Q8SWJ6 encephalito
19	292	47.4	113	4 Q9Y5M7	Q9Y5M7 homo sapien
20	292	47.4	113	4 Q9UBF6	Q9UBF6 homo sapien
21	290.5	47.2	113	11 Q9WT21	Q9WT21 mus musculu
22	266	43.2	112	5 P91404	P91404 caenorhabdi
23	263	42.7	119	5 Q95YV1	Q95YV1 leishmania
24	210	34.1	85	10 Q940X6	Q940X6 arabidopsis
25	197	32.0	85	5 Q9U1J4	Q9U1J4 drosophila
26	197	32.0	447	5 Q9YLJ5	Q9YLJ5 drosophila
27	164.5	26.7	94	3 Q9UT86	Q9UT86 schizosacch
28	146.5	23.8	135	5 Q200S2	Q200S2 caenorhabdi
29	144.5	23.5	108	4 Q9BXN8	Q9BXN8 homo sapien
30	141	22.9	57	10 Q9M9J0	Q9M9J0 arabidopsis
31	136	22.1	165	3 Q121S7	Q121S7 saccharomyc
32	134.5	21.8	54	4 Q9BM64	Q9BM64 homo sapien
33	133.5	21.7	42	11 Q9CTG0	Q9CTG0 mus musculu
34	132.5	21.5	99	10 Q9AVZ5	Q9AVZ5 guilliaridia
35	116.5	18.9	2160	5 Q17709	Q17709 caenorhabdi
36	112.5	18.3	911	3 Q96UD5	Q96UD5 neurospora
37	106.5	17.3	189	10 Q94J02	Q94J02 oryza sativ
38	106	17.2	445	12 Q8QXK0	Q8QXK0 ectocarpus
39	104	16.9	349	10 Q9S0G6	Q9S0G6 arabidopsis
40	102.5	16.6	249	10 Q9CA55	Q9CA55 arabidopsis
41	102	16.6	151	10 Q9FI95	Q9FI95 arabidopsis
42	102	16.6	210	10 Q9SD55	Q9SD55 arabidopsis
43	100	16.2	147	10 Q9LJY5	Q9LJY5 arabidopsis
44	100	16.2	676	10 Q9MIS2	Q9MIS2 arabidopsis
45	98	15.9	158	10 Q9SRM0	Q9SRM0 arabidopsis

ALIGNMENTS

RESULT 1
Q9Y254 PRELIMINARY; PRT; 108 AA.
ID Q9Y254
AC Q9Y254;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE RING finger protein (Ring-box 1).
OS ROCI OR RBX1 OR BA554C12.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP 1
RX MEDLINE-99234320; PubMed-10230407;
RA Ohta T., Michel J.J., Schottelius A.J., Xiong Y.;
RT "Roci1, a homolog of APC11, represents a family of cullin partners with
an associated ubiquitin ligase activity.";
RL Mol. Cell 3:535-541(1999). Apr
RN 2
RP 2
RX MEDLINE-99234320; PubMed-10213691;
RA Kamura T., Keop D.M., Conrad M.N., Skowrya D., Moreland R.J.,
RA Iliopoulos O., Lane W.S., Kaellin W.G. Jr., Ellledge S.D., Conaway R.C.,
RA Harper J.W., Conaway J.W.;
RT "Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase.";
RL Science 284:657-661(1999).
RN 3
RP 3
RX MEDLINE-99234320; PubMed-10213691;
RA Matthews L.;
RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RN 4
RP 4
RX MEDLINE-99234320; PubMed-10213691;
RA TISSUE-PLACENTA;
RT Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN 5

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RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF142059; AAD30146.1; -
DR EMBL: AF140598; AAD29715.1; -
DR EMBL: AL080242; CAB62925.1; -
DR EMBL: BC001466; AAH01466.1; -
DR EMBL: BC017370; AAH17370.1; -
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 108 AA; 12274 MW; 30FC5ADf66096C0E CRC64;

Query Match 100.0%; Score 616; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9e-66;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60
DB 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60

QY 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108
DB 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108

RESULT 2
QY Q9WUK9 PRELIMINARY; PRT; 108 AA.
ID Q9WUK9
AC Q9WUK9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Ring-box protein 1.
GN RBX1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99234320; PubMed-10213691;
RA Kamura T., Koop D.M., Conrad M.N., Skowrya D., Moreland R.J.,
RA Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C.,
RA Harper J.W., Conaway J.W.;
RT "RBX1, a component of the VHL tumor suppressor complex and SCF
RT ubiquitin ligase.";
RL Science 284:657-661(1999).
DR EMBL: AF140599; AAD29716.1; -
DR MGD: MGI:1891829; Rbx1.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 108 AA; 12274 MW; 30FC5ADf66096C0E CRC64;

Query Match 100.0%; Score 616; DB 11; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9e-66;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60
DB 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60

QY 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108
DB 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108

RESULT 3
QY Q9D1S2 PRELIMINARY; PRT; 108 AA.
ID Q9D1S2
AC Q9D1S2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
SQ SEQUENCE 108 AA; 12274 MW; 30FC5ADf66096C0E CRC64;
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DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 1500002P15RLK protein.
GN RBX1 OR 1500002P15RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirra L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baris G.,
RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wysshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK003159; BAB22612.1; -
DR MGD: MGI:1891829; Rbx1.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 108 AA; 12318 MW; 30FC5DA8160E1B7E CRC64;

Query Match 98.2%; Score 605; DB 11; Length 108;
Best Local Similarity 99.1%; Pred. No. 4e-65;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60
DB 1 MAAMDVPTPGSTNGACKRFEVKKNAVALMAMDIVVNDCAICRNIMDLCTECQANQ 60

QY 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108
DB 61 ASATSEECTVAMGVCNNAHFHCISRWLKTROVCPDLNREMEFOKYG 108

RESULT 4
QY Q8OG64 PRELIMINARY; PRT; 189 AA.
ID Q8OG64
AC Q8OG64;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hyperosmotic protein 21.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Prolecanthopterygii; Salmoniformes; Salmonidae; Salmo.
OC NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Pan F., Zarate J., Bradley T.M.;
RT "A homolog of the E3 ubiquitin ligase Rbx1 is induced during
RT hyperosmotic stress of salmon.";
RL Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:0-0(2002).
DR EMBL: AY027936; AAK29182.1; -
SQ SEQUENCE 189 AA; 20905 MW; 05DD44BACC095B45 CRC64;
```

Query Match 98.1%; Score 604; DB 13; Length 189;
 Best Local Similarity 98.1%; Pred. No. 9.5e-65;
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAMADVDPSTGNSGAGKREVKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 60
 |||||
 DB 82 MAAMADVDPSTGNSGAGKREVKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 141
 |||||

OY 61 ASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 108
 |||||

DB 142 ASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 189
 |||||

RESULT 5
 Q9W5E1 PRELIMINARY: PRT: 108 AA.

ID Q9W5E1
 AC Q9W5E1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE EG:115C2.11 protein.
 GN ROCI4 OR EG:115C2.11 OR CG16982.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pletlifer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhu Q., Zheng L.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003418; AAF45536.1;
 DR PLAYbase: FBgn0025638; ROCI4.
 DR InterPro: IPR001841; Znf_ring.
 DR SMART: SM00184; RING; 1.

SQ SEQUENCE 108 AA; 12538 MW; 15784198281BCD13 CRC64;
 Query Match 86.7%; Score 534; DB 5; Length 108;
 Best Local Similarity 87.2%; Pred. No. 1.4e-56;
 Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2;

OY 5 MVDV-----TPSGTNSGAGKREVKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 59
 |||||
 DB 1 MEVDDEGVEYEPSSSSNG-DKREVKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 59
 |||||

OY 60 QASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 108
 |||||
 DB 60 QASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 108
 |||||

RESULT 6
 Q8S3S0 PRELIMINARY: PRT: 114 AA.

ID Q8S3S0
 AC Q8S3S0
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative ring box-1 protein.
 GN 49d11.12.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, NIPPONBARE;
 RA Park Y.-J., Rostoks N., Ramakrishna W., Sanmiquel P., Shiloff B.,
 RA Ma J., Jiang Z., Kleinbois A., Bennetzen J.,
 RT "Sequence characterization of orthologous regions in the barley and
 rice genomes.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF480496; AAL87158.1;
 SQ SEQUENCE 114 AA; 12754 MW; 56863380D733DD5C CRC64;

Query Match 85.0%; Score 523.5; DB 10; Length 114;
 Best Local Similarity 84.4%; Pred. No. 2.7e-55;
 Matches 92; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 MAAMADVDPSTGNSGAGKREVKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 59
 |||||
 DB 6 VAAVAPPSTAGASSGAKGKREIKKNNAVALMAMDIYVNCALICRNHIMDLICICQAN 65
 |||||

OY 60 QASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 108
 |||||
 DB 66 QASATSECTVAMGVCNNAHFHFCISRWLKTROVCPILDNREMEFQYGH 114
 |||||

RESULT 7
 Q940X7 PRELIMINARY: PRT: 118 AA.

ID Q940X7
 AC Q940X7
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ring box-1-like protein (Ring-box protein-like).
 GN AT5G20570.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okresz L.,
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 2 RING-TYPE ZINC FINGERS.
 DR EMBL: AY052401; AAL13435.1; -
 DR EMBL: AY072430; AAL62422.1; -
 DR InterPro: IPR001841; Znf_fing.
 KW Zinc-finger.
 SQ SEQUENCE 118 AA; 13238 MW; 19947BF06F442A82 CRC64;

Query Match 83.5%; Score 514.5; DB 10; Length 118;
 Best Local Similarity 78.6%; Pred. No. 3.4e-54;
 Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;

OY 3 AAMDVD---PSG-----TNSGAGKKRFEVKKNVAVLAMDIVDNCALICRNHMD 51
 DB 2 ATLSDVTMIDPGEASSVVAASSSKKKRFEIKKWSAVLAMDIVDNCALICRNHMD 61
 QY 52 LCIEQANASATSECTVANGVCNHAHFHCISRWLKTROYCPLDNREMEFOKYGH 108
 DB 62 LCIEQANASATSECTVANGVCNHAHFHCISRWLKTROYCPLDNREMEFOKYGH 118

RESULT 8
 077429 PRELIMINARY; PRT; 136 AA.

AC 077429
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE EG.11SC2.11 protein.
 GN ROCI1A OR EG.11SC2.11 OR CG16982.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Salles C., Valenti P., Darlambitsou A., Henderson N., Campbell L.,
 RA Glover D.;
 RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL031581; CAA20888.1; -
 DR FLYBase: FBgn0025638; Roci1a.
 DR InterPro: IPR001841; Znf_fing.
 DR SMART: SM00184; RING; 1.
 SQ SEQUENCE 136 AA; 15656 MW; 80812FA428A51EA7 CRC64;

Query Match 82.8%; Score 510; DB 5; Length 136;
 Best Local Similarity 69.3%; Pred. No. 1.4e-53;
 Matches 95; Conservative 4; Mismatches 4; Indels 34; Gaps 3;

OY 5 MDVD-----TPSGTNSGAKRFEVKK-----WNAVA 31
 DB 1 MEVEDGTEVSSSSKG-DKRRFEVKKVSQOKSRVINECTDGTSTFPLRRQWNAVA 59
 QY 32 LMAWDIVDNCALICRNHMDICIEQANASATSECTVANGVCNHAHFHCISRWLKT 91
 DB 60 LMAWDIVDNCALICRNHMDICIEQANASATSECTVANGVCNHAHFHCISRWLKT 119
 QY 92 QVCPDLNREMEFOKYGH 108
 DB 120 QVCPDLNREMEFOKYGH 136

RESULT 9
 OY9M2B0 PRELIMINARY; PRT; 115 AA.

AC 09M2B0
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Ring-box protein-like.
 GN T21C14-50.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Delseny M., Berger C., Cooke R., Gaubier P., Grellet F., Laudie M.,
 RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
 RA Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL138639; CAB87200.1; -
 DR InterPro: IPR001841; Znf_fing.
 DR SMART: SM00184; RING; 1.
 SQ SEQUENCE 115 AA; 12999 MW; 1515E3E417DB1FAF CRC64;

Query Match 81.0%; Score 499; DB 10; Length 115;
 Best Local Similarity 81.5%; Pred. No. 2.4e-52;
 Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

OY 1 MAAMDVDPSGTCNSGAKRFEVKKNVAVLAMDIVDNCALICRNHMDICIEQANO 60
 DB 10 MCESSISVPS--SSSKSKRELKWSAVLAMDIVDNCALICRNHMDICIECLANO 67
 QY 61 ASATSECTVANGVCNHAHFHCISRWLKTROYCPLDNREMEFOKYGH 108
 DB 68 ASATSECTVANGVCNHAHFHCISRWLKTROYCPLDNREMEFOKYGH 115

RESULT 10
 Q23457 PRELIMINARY; PRT; 110 AA.

AC Q23457
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ZK287.5 protein.
 GN ZK287.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitidae;
 OC Rhabdilitae; Peloderiinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99069613; PubMed-9851916;
 RX none;
 RA none;

RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z70757; CAA94801.1; -
 DR InterPro: IPR001841; Znf_fing.
 DR SMART: SM00184; RING; 1.
 SQ SEQUENCE 110 AA; 12760 MW; EEE50F7684B30A56 CRC64;

Query Match 80.0%; Score 493; DB 5; Length 110;

[illegible]

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha

Muscomorpha;

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OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Abmayyan A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melnikov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brockstein P., Hong L., Abmayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Garlin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003468; AAF47382.1; -
DR EMBL; AY070810; AAL48432.1; -
DR FLYBase; FBgn0040291; Rocl.b.
DR InterPro; IPR001841; znf_ring.
DR SMART; SM00184; RING; 1.
SO SEQUENCE 122 AA; 14225 MW; F22CE00438725410 CRC64;

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Query Match          65.0%; Score 400.5; DB 5; Length 122;
Best Local Similarity 65.4%; Pred. No. 1.8e-40;
Matches 70; Conservative 13; Mismatches 19; Indels 5; Gaps 2;

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OY 5 MDVDTPSGTSNG---AGKKREYKKNNAVALMWDIVVNCALICRNHIMDLCTECQANO 60
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 16 MDFNDEBSPSCGAVGARTERFVVKVVAHAMMGWDVAVDNCALICRNHIMDLCTECQAD 74
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
OY 61 ASATSEECTVAMGVCNNAHFHFCISRWLKTROVCPLDNREWEFOKYG 107
   :  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 75 PNANODECTVAMGVCNNAHFHFCISRWLKTROVCPLDNREWEFOKYG 121
   :  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :

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RESULT 15

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008273
AC Q08273 PRELIMINARY; PRT; 121 AA.
ID Q08273;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ORF YOL133W.
GN HRT1 OR YOL133W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Arino J., Casamayor A., Gamo F.J., Gancedo C., Lafuente M.J.,
RA Aldea M., Casas C., Herrero E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL MIPS;
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=97051593; PubMed=8896270;
RA Aldea M., Piedralita L., Casas C., Casamayor A., Khalid H.,
RA Balcells L., Arino J., Herrero E.;
RT "Sequence analysis of a 12 801 bp fragment of the left arm of yeast
RT chromosome XV containing a putative 6-phosphofructo-2-kinase gene, a
RT gene for a possible glycopospholipid-anchored surface protein and six
RT other open reading frames.";
RL Yeast 12:1053-1058(1996).
DR EMBL; Z74876; CAA99155.1; -
DR EMBL; X95465; CAA64737.1; -
DR SGD; S0005493; HRT1.
DR InterPro; IPR001841; znf_ring.
DR SMART; SM00184; RING; 1.
SO SEQUENCE 121 AA; 13940 MW; A9C3193E48CAF881 CRC64;

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Query Match          62.5%; Score 385; DB 3; Length 121;
Best Local Similarity 56.6%; Pred. No. 1.3e-38;
Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;

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Search completed: May 11, 2003, 02:11:30
Job time : 73 secs

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OY 5 MDVDTPSGTSNGAG-----KKREYKKNNAVALMWDIVVNCALICRNHIMDLCT 54
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 8 MDVDEDESQNTIAOSSNOSGAPVETKKKKREIKKWTAVAFMSWDIADNCALICRNHIMEPCI 67
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
OY 55 ECQANQASATSEECTVAMGVCNNAHFHFCISRWLKTROVCPLDNREWEFOKYG 107
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 68 ECQPRAMTDTDNECVAMGVCNNAHFHFCINKNWIKTRDACPILDNPPWOLARCG 120
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :

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